

SEQUENCE LISTING

<110> KIZAKI, NORIYUKI
YASOHARA, YOSHIHIKO
HASEGAWA, JUNZO

<120> NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

<130> 025835/0104

<140> 10/088,920

<141> 2002-06-03

<150> PCT/JP01/06619

<151> 2001-08-01

<150> JP 2000-232756

<151> 2000-08-01

<160> 11

<210> 1

<211> 277

<212> PFT

<213> Micrococcus luteus

<400> 1

Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly
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Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu
20 25 30

Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp
35 40 45

Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu
50 55 60

Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met
65 70 75 80

Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser
85 90 95

Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp
100 105 110

Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu
115 120 125

Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His
130 135 140

Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr
145 150 155 160

Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp
 165 170 175

Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser
 180 185 190

Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val
 195 200 205

Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Leu Ala Trp Val
 210 215 220

Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
 225 230 235 240

His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
 245 250 255

Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
 260 265 270

Pro Leu Glu Met Leu
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<210> 2
 <211> 1410
 <212> DNA
 <213> Micrococcus luteus

<220>
 <221> CDS
 <222> (108)..(938)

<400> 2
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ctcagcccccac gtcccgccctc aggacaacca gaaggaagtg atcgcggt atg cga cgg 116
 Met Arg Arg
 1

atg acg ctg ccg agt ggg gag tcc atc cct gtg ctg ggc cag ggc acc 164
 Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly Gln Gly Thr
 5 10 15

tgg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag gtc gcc gcg 212
 Arg Arg Arg Arg Arg Asp Pro Gly Arg Arg Gly Asp Gln Val Ala Ala
 20 25 30 35

ctg cac gcc ggc ctc gag ctg ggc atg acg ctg gtc gac acc gcc gag 260
 Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp Thr Ala Glu
 40 45 50

atg tac gcc gac ggc ggt gcg gag gag gtg gct ggt gaa gca ttg gcg 308
 Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu Ala Leu Ala
 55 60 65

ggt cgc cgc gac gag gcg ttc gtg gtc agc aag gtc atg ccg tcc cac 356
 Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met Pro Ser His
 70 75 80

gcc tcc cgt tcc ggc acg atc gcg gcc tgc gaa cgc agc ctg aaa cgc 404
 Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser Leu Lys Arg
 85 90 95

ctg ggc acc gat cgg atc gac ctc tac ctg ctg cac tgg cag ggc agg 452
 Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp Gln Gly Arg
 100 105 110 115

tac ccg ctg cag gac acc gtc gcg gcc ttc cac cag ctc gtc gag gac 500
 Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu Val Glu Asp
 120 125 130

ggg aaa atc cga tac tgg ggc gtc agc aac ttc gac cac cgg gcc ctc 548
 Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His Arg Ala Leu
 135 140 145

gcc gag ctg cag gac gtg ccg ggc acc agc ggg ctg acc acg gat cag 596
 Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr Thr Asp Gln
 150 155 160

gtg ctg tac aac ctg tcg cgg cga gga ccg gag tac gac ctg ctg ccg 644
 Val Leu Tyr Asn Leu Ser Arg Gly Pro Glu Tyr Asp Leu Leu Pro
 165 170 175

tgg tgc gcc gac cac cag ctg ccg gtc atg gcg tac tcg ccg atc gag 692
 Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser Pro Ile Glu
 180 185 190 195

cag ggc cgc atc ctt gac gac acg acg ctg aac gac gtc gcg gcc cgt 740
 Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val Ala Ala Arg
 200 205 210

cac agc gtc agc ccc gcg gcg gcg gcc ctt gcc tgg gtg ctg cgc cgc 786
 His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val Leu Arg Arg
 215 220 225

gac tcg ctc tgc acg atc ccc aag gcg agc agc ccg cag cac gtg cgc 836
 Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln His Val Arg
 230 235 240

gac aac gcc aca gca ctg gac gtg gag ctg acc cgc gaa gac ctg gat 864
 Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu Asp Leu Asp
 245 250 255

jct ctg gac cgt ggg ttt ccg ccc ccg agc gga ccg cga cca ctg gaa 884
 Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg Pro Leu Glu
 260 265 270 275

atg ctg tgacctgcc ccagggcgca gccgggtcgg tccggggcggt ccgggcagtc 980
 Met Leu

cgggtagcgc tccggtcagc gcaagtctcc gaaggacctg cctgtcacct cctcctgaac 1048

ctgtgcacgc catccatcga ctcccttctc cgagccctgt cgggttcgcg gtaggcgctg 1108

atcatccgct ggcagggtccc ccaagtggcc tcgagccggg ccctctgctt gtcggtgagc 1168
 aaccgggttc cggcgtgcag ggttcgacgg gcggagtaga gcgggtcgcc cgtgcgggccc 1228
 cgggtggccat gcagggtcctg ctggacccgg cgggtggcagc ggaccaacgc gtcgccgggt 1288
 aaccggactg cgagcgaccg gcgttgtgga cgcagacgac ctggacactg ggccgtgcgg 1348
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 tc 1410

<210> 3
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (6)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (9)
 <223> a, t, c, g, other or unknown

<400> 3
 gayaacngcng aratgtaygc 20

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (6)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (9)
 <223> a, t, c, g, other or unknown

<400> 4
 tcytcnacna gytgrtgraa 20

<210> 5
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 gcgcatatgc gacggatgac gctgcc 26

<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 ggogaattct tacagcattt ccagtggtcg cg 32

<210> 7
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 gcgaattcta aggagattta tatatgacgac ggatgacgct gccgag 46

<210> 8
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
 caggagctct tacagcattt ccagtggtc 29

<210> 9
 <211> 144
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 double-stranded DNA

<400> 9
 gaattctaag gagatttaca tatgcgtcgt atgactttac catctgggtga atctattcca 60
 gttttagggtc aagggtacttg gggttgggggt gaagatccag gtcgtcgtgg tgatgaagtt 120
 gctgctttac atgctqgtct cgag 144

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 10
 caggagctct aaggagggtta acaatgtata aag 33

<210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 11
 cacggatcct tatccgcgtc ctgcttgg 28